

results of BLAST

BLASTN 2.2.6 [Apr-09-2003]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1057611986-09423-8321

Query=

(18 letters)

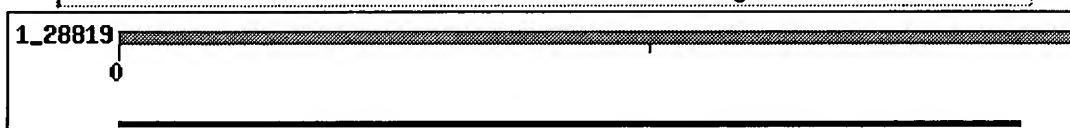
Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences)
1,833,629 sequences; 8,583,520,539 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 1 Blast Hits on the Query Sequence

Mouse-over to show define and scores. Click to show alignments



Sequences producing significant alignments:

Score E
(bits) Value

[gi|35841|emb|X03484.1|HSRAFR](#) Human mRNA for raf oncogene

36 4e-07

Alignments

Get selected sequences

Select all

Deselect all

☐ [>gi|35841|emb|X03484.1|HSRAFR](#) Human mRNA for raf oncogene
Length = 2977

Score = 36.2 bits (18), Expect = 4e-07
Identities = 18/18 (100%)
Strand = Plus / Minus

Query: 1 tccctgtatgtgctccat 18

|||||
Sbjct: 147 tccctgtatgtgctccat 130

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS,
or phase 0, 1 or 2 HTGS sequences)

Posted date: Jul 6, 2003 10:33 PM

Number of letters in database: -24,356,671

Number of sequences in database: 1,826,964

Lambda	K	H
1.37	0.711	1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3

Gap Penalties: Existence: 5, Extension: 2

Number of Hits to DB: 1

Number of Sequences: 6665

Number of extensions: 1

Number of successful extensions: 1

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 1

length of query: 18

length of database: 2977

effective HSP length: 7

effective length of query: 11

effective length of database: 2970

effective search space: 32670

effective search space used: 32670

T: 0

A: 0

X1: 6 (11.9 bits)

X2: 15 (29.7 bits)

S1: 12 (24.3 bits)

S2: 6 (12.4 bits)